



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 162513

TO: Joseph F Murphy  
Location: REM/4D78/4C70  
Art Unit: 1646  
Thursday, August 18, 2005  
  
Case Serial Number: 09/765534

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512  
  
edward.hart@uspto.gov

### Search Notes

Examiner Murphy,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

162513

From: Murphy, Joseph  
Sent: Monday, August 15, 2005 11:07 AM  
To: STIC-Biotech/ChemLib  
Subject: 09765534

STIC/Biotech:

Please do an oligo search of SEQ ID NO: 2, 4.

Please include an interference search.

Please send the results on DISK.

Thanks a lot...

Joseph F. Murphy, Ph.D.  
Primary Examiner, Art Unit 1646  
joseph.murphy@uspto.gov  
Remsen 4D78  
Mailbox: 4C70  
(571) 272-0877

\*\*\*\*\*

STAFF USE ONLY

Searcher: Hart  
Searcher Phone: 2-  
Date Searcher Picked up: 8/17/05  
Date Completed: 8/17/05  
Searcher Prep/Rev. Time:         
Online Time:       

\*\*\*\*\*

Type of Search

NA#:        AA#: 2  
Interference:        SPDI:         
S/L:        Oligomer:         
Encode/Transl:         
Structure#:        Text:         
Inventor:        Litigation:       

\*\*\*\*\*

Vendors and cost where applicable

STN:         
DIALOG:         
QUESTEL/ORBIT:         
LEXIS/NEXIS:         
SEQUENCE SYSTEM: 22P  
WWW/Internet:         
Other(Specify):

# 09765534 Resultsoligo

SEQ ID NO: 2

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6857	100.0	1298	2	AAR85937	Aar85937 Protein t
2	6857	100.0	1298	2	AAR90528	Aar90528 FLT4 rece
3	6857	100.0	1298	2	ADP90836	Adp90836 Human fms
4	6857	100.0	1298	3	AAY90365	Aay90365 Human Flt
5	6857	100.0	1298	3	AAY70746	Aay70746 Human tyr
6	6857	100.0	1298	5	ABG32043	Abg32043 Human Flt
7	6857	100.0	1298	6	ABU04292	Abu04292 Human exp
8	6857	100.0	1298	6	ABU04307	Abu04307 Human exp
9	6857	100.0	1298	6	ABU04296	Abu04296 Human exp
10	6857	100.0	1298	6	ABU04274	Abu04274 Human exp
11	6857	100.0	1298	6	ABU04294	Abu04294 Human exp
12	6857	100.0	1298	6	ABU04293	Abu04293 Human exp
13	6857	100.0	1298	7	ADD08956	Add08956 Human VEG
14	6857	100.0	1298	7	ADF45098	Adf45098 Human kin
15	6857	100.0	1304	6	ABU04279	Abu04279 Human exp
16	6852	99.9	1363	2	ADP90838	Adp90838 Human fms
17	6852	99.9	1363	3	AAY90366	Aay90366 Human Flt
18	6852	99.9	1363	3	AAY70747	Aay70747 Human tyr
19	6852	99.9	1363	3	AAB29047	Aab29047 Human Flt
20	6852	99.9	1363	4	AAB37604	Aab37604 Human Flt
21	6852	99.9	1363	5	ABG32044	Abg32044 Human Flt
22	6852	99.9	1363	6	ABU04297	Abu04297 Human exp
23	6852	99.9	1363	6	ABU04284	Abu04284 Human exp
24	6852	99.9	1363	6	ABU04282	Abu04282 Human exp
25	6852	99.9	1363	6	ABU04295	Abu04295 Human exp
26	6813	99.4	1298	4	AAY97785	Aay97785 Mouse Flt
27	6813	99.4	1298	4	AAY97575	Aay97575 Human Flt
28	6813	99.4	1298	6	ABU07853	Abu07853 Human vas
29	6813	99.4	1298	6	ABU04298	Abu04298 Human exp
30	6813	99.4	1298	6	ABU04304	Abu04304 Human exp
31	6813	99.4	1298	6	ABU04277	Abu04277 Human exp
32	6813	99.4	1298	7	ADN95352	Adn95352 Human BEC
33	6813	99.4	1298	8	ADQ91191	Adq91191 Human vas
34	6813	99.4	1298	8	ADR05211	Adr05211 Human fms
35	6808	99.3	1363	7	ADC64992	Adc64992 Human VEG
36	6796	99.1	1298	3	AAB30542	Aab30542 Amino aci
37	6796	99.1	1298	6	ABU04283	Abu04283 Human exp
38	6073	88.6	1363	4	AAB37607	Aab37607 Human pro
39	6073	88.6	1363	6	ABU04285	Abu04285 Human exp
40	2754.5	40.2	1356	4	AAB62475	Aab62475 Human VEG
41	2754.5	40.2	1356	4	AAY97576	Aay97576 Human Flk
42	2754.5	40.2	1356	6	ABR40196	Abr40196 Human vas
43	2754.5	40.2	1356	7	ADD08954	Add08954 Human VEG
44	2754.5	40.2	1356	7	ABM79007	Abm79007 Human VEG
45	2754.5	40.2	1356	7	ADF45097	Adf45097 Human kin

Issued Patents:

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6857	100.0	1298	1	US-08-222-616-33	Sequence 33, Appl
2	6857	100.0	1298	1	US-08-340-011-2	Sequence 2, Appli
3	6857	100.0	1298	3	US-08-901-710-2	Sequence 2, Appli
4	6857	100.0	1298	3	US-08-446-648-33	Sequence 33, Appl
5	6857	100.0	1298	4	US-09-982-610-33	Sequence 33, Appl

6	6857	100.0	1298	4	US-09-169-079-2	Sequence 2, Appli
7	6857	100.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl
8	6852	99.9	1363	1	US-08-340-011-4	Sequence 4, Appli
9	6852	99.9	1363	3	US-08-901-710-4	Sequence 4, Appli
10	6852	99.9	1363	4	US-09-375-248-2	Sequence 2, Appli
11	6852	99.9	1363	4	US-09-169-079-4	Sequence 4, Appli
12	6798	99.1	1363	2	US-08-874-678-32	Sequence 32, Appl
13	6798	99.1	1363	3	US-08-643-839-32	Sequence 32, Appl
14	6798	99.1	1363	3	US-09-348-886-32	Sequence 32, Appl
15	6438.5	93.9	1368	2	US-08-874-678-34	Sequence 34, Appl
16	6438.5	93.9	1368	3	US-08-643-839-34	Sequence 34, Appl
17	6438.5	93.9	1368	3	US-09-348-886-34	Sequence 34, Appl

RESULT 1

US-08-222-616-33

; Sequence 33, Application US/08222616

; Patent No. 5635177

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/222,616

; FILING DATE: 4-APR-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/00586

; FILING DATE: 22-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/826935

; FILING DATE: 22-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 821P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-222-616-33

Query Match 100.0%; Score 6857; DB 1; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLSISCRGQHPLEWA	60
Db	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLSISCRGQHPLEWA	60
Qy	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Db	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Db	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Db	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Qy	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSFHALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNVV	420
Db	361	YPPPEFQWYKDGKALSGRHSFHALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNVV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQRSLRRRQQQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQRSLRRRQQQ	480
Qy	481	DLMPQCRDWRVATTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVVSAMYKCVVSNKV	540
Db	481	DLMPQCRDWRVATTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVVSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLSCQADSYKYEHLRWYRLNLSTLHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLSCQADSYKYEHLRWYRLNLSTLHD	600
Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080

Qy 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Db 1081 MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA 1140  
 |||||  
 Qy 1141 TPAIRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
 |||||  
 Db 1141 TPAIRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS 1200  
 |||||  
 Qy 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEEFPM 1260  
 |||||  
 Db 1201 QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEEFPM 1260  
 |||||  
 Qy 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFR 1298  
 |||||  
 Db 1261 TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFR 1298  
 |||||

RESULT 4

US-08-446-648-33

; Sequence 33, Application US/08446648

; Patent No. 6331302

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,648

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-446-648-33

Query Match 100.0%; Score 6857; DB 3; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1x 58-69, 113

7

RESULT 5

US-09-982-610-33

; Sequence 33, Application US/09982610

; Patent No. 6673343

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; Bennett, Brian D.  
; Goeddel, David  
; Lee, James M.  
; Matthews, William  
; Tsai, Siao Ping  
; Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/982,610  
; FILING DATE: 17-Oct-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/446,648  
; FILING DATE: 1996-MAY-23  
; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1298 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-982-610-33

Query Match 100.0%; Score 6857; DB 4; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

PCT-US95-04228-33

; Sequence 33, Application PC/TUS9504228

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04228  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/222616  
 ; FILING DATE: 04-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wendy M. Lee  
 ; REGISTRATION NUMBER: 00,000  
 ; REFERENCE/DOCKET NUMBER: 821P3PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 33:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1298 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 PCT-US95-04228-33

Query Match 100.0%; Score 6857; DB 5; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 US-08-874-678-32  
 ; Sequence 32, Application US/08874678  
 ; Patent No. 5952199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis-Smyth, Terri L.  
 ; APPLICANT: Chen, Helen H.  
 ; APPLICANT: Presta, Leonard  
 ; APPLICANT: Fexrara, Napoleone  
 ; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
 ; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/874,678  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/643,839  
 ; FILING DATE: 07-MAY-1996

5-7-96



; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-63291-1/WH  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1363 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 US-08-874-678-32

Query Match 99.1%; Score 6798; DB 2; Length 1363;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 1288; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

PGPUBS:

# SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	6857	100.0	1298	9	US-09-982-610-33 Sequence 33, Appl
2	6857	100.0	1298	11	US-09-765-534B-2 Sequence 2, Appli
3	6857	100.0	1298	14	US-10-262-538-32 Sequence 32, Appl
4	6857	100.0	1298	15	US-10-394-322A-67 Sequence 67, Appl
5	6857	100.0	1298	16	US-10-774-802-2 Sequence 2, Appli
6	6857	100.0	1298	16	US-10-669-176-32 Sequence 32, Appl
7	6857	100.0	1298	16	US-10-473-127-940 Sequence 940, App
8	6857	100.0	1298	16	US-10-473-127-958 Sequence 958, App
9	6857	100.0	1298	16	US-10-473-127-959 Sequence 959, App
10	6857	100.0	1298	16	US-10-473-127-960 Sequence 960, App
11	6857	100.0	1298	16	US-10-473-127-962 Sequence 962, App
12	6857	100.0	1298	16	US-10-473-127-973 Sequence 973, App
13	6857	100.0	1304	16	US-10-473-127-945 Sequence 945, App
14	6852	99.9	1363	10	US-09-375-248-2 Sequence 2, Appli
15	6852	99.9	1363	11	US-09-765-534B-4 Sequence 4, Appli
16	6852	99.9	1363	15	US-10-661-740-2 Sequence 2, Appli
17	6852	99.9	1363	16	US-10-774-802-4 Sequence 4, Appli
18	6852	99.9	1363	16	US-10-473-127-948 Sequence 948, App
19	6852	99.9	1363	16	US-10-473-127-950 Sequence 950, App
20	6852	99.9	1363	16	US-10-473-127-961 Sequence 961, App
21	6852	99.9	1363	16	US-10-473-127-963 Sequence 963, App
22	6813	99.4	1298	15	US-10-165-193A-12 Sequence 12, Appl
23	6813	99.4	1298	16	US-10-326-048-4 Sequence 4, Appli
24	6813	99.4	1298	16	US-10-473-127-943 Sequence 943, App
25	6813	99.4	1298	16	US-10-473-127-964 Sequence 964, App
26	6813	99.4	1298	16	US-10-473-127-970 Sequence 970, App
27	6813	99.4	1298	17	US-10-781-581-222 Sequence 222, App
28	6808	99.3	1363	14	US-10-081-126-2 Sequence 2, Appli
29	6798	99.1	1363	14	US-10-105-901-32 Sequence 32, Appl
30	6796	99.1	1298	16	US-10-473-127-949 Sequence 949, App
31	6438.5	93.9	1368	14	US-10-105-901-34 Sequence 34, Appl
32	6073	88.6	1363	10	US-09-375-248-19 Sequence 19, Appl
33	6073	88.6	1363	15	US-10-661-740-19 Sequence 19, Appl
34	6073	88.6	1363	16	US-10-473-127-951 Sequence 951, App
35	5646.5	82.3	1362	14	US-10-105-901-33 Sequence 33, Appl
36	4135	60.3	777	14	US-10-105-901-3 Sequence 3, Appli
37	2754.5	40.2	1356	14	US-10-090-183-2 Sequence 2, Appli
38	2754.5	40.2	1356	15	US-10-394-322A-66 Sequence 66, Appl
39	2754.5	40.2	1356	15	US-10-440-464-129 Sequence 129, App
40	2754.5	40.2	1356	16	US-10-783-528-61 Sequence 61, Appl
41	2754.5	40.2	1356	17	US-10-872-198-115 Sequence 115, App
42	2754.5	40.2	1356	17	US-10-741-600-1469 Sequence 1469, Ap

43	2754.5	40.2	1356	17	US-10-741-600-1471	Sequence 1471, Ap
44	2754.5	40.2	1356	17	US-10-926-806-10	Sequence 10, Appl
45	2754.5	40.2	1356	20	US-11-021-951-115	Sequence 115, App

RESULT 1

US-09-982-610-33

; Sequence 33, Application US/09982610

; Patent No. US20020146420A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
 ; Bennett, Brian D.  
 ; Goeddel, David  
 ; Lee, James M.  
 ; Matthews, William  
 ; Tsai, Siao Ping  
 ; Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/982,610  
 ; FILING DATE: 17-Oct-2001  
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/446,648  
 ; FILING DATE: 1996-MAY-23  
 ; APPLICATION NUMBER: 08/222616  
 ; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER: 40,378  
 ; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1298 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-982-610-33

Query Match 100.0%; Score 6857; DB 9; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

US-10-394-322A-67

; Sequence 67, Application US/10394322A

; Publication No. US20030232391A1

; GENERAL INFORMATION:

; APPLICANT: SUNESIS PHARMACEUTICALS, INC.

; APPLICANT: Prescott, John C.

; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS

; FILE REFERENCE: 39750-0006 US  
; CURRENT APPLICATION NUMBER: US/10/394,322A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,892  
; PRIOR FILING DATE: 2002-03-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 1298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-322A-67

Query Match 100.0%; Score 6857; DB 15; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
US-10-473-127-960  
; Sequence 960, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 960  
; LENGTH: 1298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-960

3-28-01

Query Match 100.0%; Score 6857; DB 16; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# SEQ ID NO: 4

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	7211	100.0	1363	2	ADP90838	Adp90838 Human fms
2	7211	100.0	1363	3	AAY90366	Aay90366 Human Flt
3	7211	100.0	1363	3	AAY70747	Aay70747 Human tyr
4	7211	100.0	1363	3	AAB29047	Aab29047 Human Flt
5	7211	100.0	1363	4	AAB37604	Aab37604 Human Flt
6	7211	100.0	1363	5	ABG32044	Abg32044 Human Flt
7	7211	100.0	1363	6	ABU04297	Abu04297 Human exp
8	7211	100.0	1363	6	ABU04284	Abu04284 Human exp
9	7211	100.0	1363	6	ABU04282	Abu04282 Human exp
10	7211	100.0	1363	6	ABU04295	Abu04295 Human exp
11	7167	99.4	1363	7	ADC64992	Adc64992 Human VEG
12	6852	95.0	1298	2	AAR85937	Aar85937 Protein t
13	6852	95.0	1298	2	AAR90528	Aar90528 FLT4 rece
14	6852	95.0	1298	2	ADP90836	Adp90836 Human fms
15	6852	95.0	1298	3	AAY90365	Aay90365 Human Flt
16	6852	95.0	1298	3	AAY70746	Aay70746 Human tyr
17	6852	95.0	1298	5	ABG32043	Abg32043 Human Flt
18	6852	95.0	1298	6	ABU04292	Abu04292 Human exp
19	6852	95.0	1298	6	ABU04307	Abu04307 Human exp
20	6852	95.0	1298	6	ABU04296	Abu04296 Human exp
21	6852	95.0	1298	6	ABU04274	Abu04274 Human exp
22	6852	95.0	1298	6	ABU04294	Abu04294 Human exp
23	6852	95.0	1298	6	ABU04293	Abu04293 Human exp
24	6852	95.0	1298	7	ADD08956	Add08956 Human VEG
25	6852	95.0	1298	7	ADF45098	Adf45098 Human kin
26	6852	95.0	1304	6	ABU04279	Abu04279 Human exp
27	6808	94.4	1298	4	AAY97785	Aay97785 Mouse Flt
28	6808	94.4	1298	4	AAY97575	Aay97575 Human Flt
29	6808	94.4	1298	6	ABU07853	Abu07853 Human vas
30	6808	94.4	1298	6	ABU04298	Abu04298 Human exp
31	6808	94.4	1298	6	ABU04304	Abu04304 Human exp
32	6808	94.4	1298	6	ABU04277	Abu04277 Human exp
33	6808	94.4	1298	7	ADN95352	Adn95352 Human BEC
34	6808	94.4	1298	8	ADQ91191	Adq91191 Human vas
35	6808	94.4	1298	8	ADR05211	Adr05211 Human fms
36	6791	94.2	1298	3	AAB30542	Aab30542 Amino aci
37	6791	94.2	1298	6	ABU04283	Abu04283 Human exp
38	6320	87.6	1363	4	AAB37607	Aab37607 Human pro
39	6320	87.6	1363	6	ABU04285	Abu04285 Human exp
40	2762	38.3	1356	4	AAB62475	Aab62475 Human VEG
41	2762	38.3	1356	4	AAY97576	Aay97576 Human Flk
42	2762	38.3	1356	6	ABR40196	Abr40196 Human vas
43	2762	38.3	1356	7	ADD08954	Add08954 Human VEG
44	2762	38.3	1356	7	ABM79007	Abm79007 Human VEG
45	2762	38.3	1356	7	ADF45097	Adf45097 Human kin

## RESULT 2

### AAY90366

ID AAY90366 standard; protein; 1363 AA.

XX

AC AAY90366;

XX

DT 15-JAN-2001 (first entry)

XX

DE Human Flt4 receptor tyrosine kinase long form protein sequence.

XX

KW Human; Flt4 receptor tyrosine kinase; antibody; extracellular domain;

KW lymphatic vessel detection; lymphatic tissue; lymph node tissue;

KW endothelial venule; diagnosis; lymphoma; long form.

XX  
 OS Homo sapiens.  
 XX  
 PN US6107046-A.  
 XX  
 PD 22-AUG-2000.  
 XX  
 PF 28-JUL-1997; 97US-00901710.  
 XX  
 PR 09-OCT-1992; 92US-00959951.  
 PR 09-JUN-1994; 94US-00257754.  
 PR 14-NOV-1994; 94US-00340011.  
 XX  
 PA (ORIN ) ORION CORP.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;  
 PI Matikainen M, Pajusola K;  
 XX  
 DR WPI; 2000-571323/53.  
 DR N-PSDB; AAA37816.  
 XX  
 PT Antibody to extracellular domain of or to an epitope unique to a  
 PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing  
 PT lymphoma and imaging lymphatic vessels or high endothelial venules in  
 PT tissue.  
 XX  
 PS Claim 21; Col 55-66; 66pp; English.  
 XX  
 CC This sequence represents the human Flt4 receptor tyrosine kinase long  
 CC form protein. The invention relates to an antibody (I) specific to the  
 CC extracellular domain of or to an epitope unique to a vertebrate Flt4  
 CC receptor tyrosine kinase protein (II). A composition comprising (I) is  
 CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph  
 CC node tissue or high endothelial venules in an organism preferably mammal  
 CC especially human. The method comprises administering the composition and  
 CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high  
 CC endothelial venules. (I) is also useful for screening a biological sample  
 CC for the presence of (II) or diagnosing a disease state. The diagnosing  
 CC method of the disease state preferably lymphoma comprises obtaining a  
 CC tissue sample on a vertebrate organism suspected of being in a diseased  
 CC state characterised by in Flt4 expression in lymphatic cells or high  
 CC endothelial venules and screening the diseased state utilising (I). (I)  
 CC is also useful for imaging lymphatic vessels or high endothelial venules  
 CC in a tissue by contacting the tissue with (I) and imaging the vessels by  
 CC detecting (I) bound to the tissues  
 XX  
 SQ Sequence 1363 AA;

Query Match 100.0%; Score 7211; DB 3; Length 1363;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 12

AAR85937

ID AAR85937 standard; protein; 1298 AA.

XX

AC AAR85937;

XX

DT 14-FEB-1996 (first entry)

XX

DE Protein tyrosine-kinase SAL-S1.

XX

KW Protein tyrosine-kinase; SAL-S1; cell growth; differentiation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= Sig\_peptide

FT Domain 25. .775  
 FT /label= Extracellular\_domain  
 FT Domain 776. .800  
 FT /label= Transmembrane\_domain  
 FT Domain 801. .1298  
 FT /label= Cytoplasmic\_tyrosine\_kinase\_domain  
 XX  
 PN WO9527061-A1.  
 XX  
 PD 12-OCT-1995.  
 XX  
 PF 04-APR-1995; 95WO-US004228.  
 XX  
 PR 04-APR-1994; 94US-00222616.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP, Wood WI;  
 XX  
 DR WPI; 1995-366160/47.  
 DR N-PSDB; AAT03090.  
 XX  
 PT Agonist antibodies which activate specific protein tyrosine kinase(s) -  
 PT also activate chimeric proteins of kinase extracellular domain and Ig  
 PT constant domain, useful for studying, and therapeutic modulation of, cell  
 PT growth and differentiation.  
 XX  
 PS Disclosure; Fig 15A-F; 125pp; English.  
 XX  
 CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used to  
 CC screen cDNA libraries to identify novel pTK genes. The SAL-S1 gene was  
 CC isolated from several megakaryocytic cell line libraries. The gene (see  
 CC AAT03090) encodes a protein (AAR85937) showing homology to FLT/FLK family  
 CC pTKs. SAL-S1 can be used to target proteins in drug design, as an  
 CC (ant)agonist of other pTKs, to screen pTK ligands or to modulate  
 CC megakaryocyte/platelet adhesion  
 XX  
 SQ Sequence 1298 AA;

Query Match 95.0%; Score 6852; DB 2; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

#### Issued Patents:

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	7211	100.0	1363	1	US-08-340-011-4	Sequence 4, Appli
2	7211	100.0	1363	3	US-08-901-710-4	Sequence 4, Appli
3	7211	100.0	1363	4	US-09-375-248-2	Sequence 2, Appli
4	7211	100.0	1363	4	US-09-169-079-4	Sequence 4, Appli
5	7157	99.3	1363	2	US-08-874-678-32	Sequence 32, Appl
6	7157	99.3	1363	3	US-08-643-839-32	Sequence 32, Appl
7	7157	99.3	1363	3	US-09-348-886-32	Sequence 32, Appl
8	6852	95.0	1298	1	US-08-222-616-33	Sequence 33, Appl
9	6852	95.0	1298	1	US-08-340-011-2	Sequence 2, Appli
10	6852	95.0	1298	3	US-08-901-710-2	Sequence 2, Appli
11	6852	95.0	1298	3	US-08-446-648-33	Sequence 33, Appl
12	6852	95.0	1298	4	US-09-982-610-33	Sequence 33, Appl
13	6852	95.0	1298	4	US-09-169-079-2	Sequence 2, Appli
14	6852	95.0	1298	5	PCT-US95-04228-33	Sequence 33, Appl
15	6797.5	94.3	1368	2	US-08-874-678-34	Sequence 34, Appl
16	6797.5	94.3	1368	3	US-08-643-839-34	Sequence 34, Appl
17	6797.5	94.3	1368	3	US-09-348-886-34	Sequence 34, Appl
18	6320	87.6	1363	4	US-09-375-248-19	Sequence 19, Appl
19	6005.5	83.3	1362	2	US-08-874-678-33	Sequence 33, Appl
20	6005.5	83.3	1362	3	US-08-643-839-33	Sequence 33, Appl

21	6005.5	83.3	1362	3	US-09-348-886-33	Sequence 33, Appl
22	4135	57.3	777	2	US-08-874-678-3	Sequence 3, Appli
23	4135	57.3	777	3	US-08-643-839-3	Sequence 3, Appli
24	4135	57.3	777	3	US-09-348-886-3	Sequence 3, Appli
25	2762	38.3	1356	4	US-09-949-016-6198	Sequence 6198, Ap
26	2762	38.3	1456	4	US-09-949-016-9853	Sequence 9853, Ap
27	2759	38.3	1356	3	US-09-098-707A-2	Sequence 2, Appli
28	2759	38.3	1356	3	US-09-483-539-2	Sequence 2, Appli
29	2753	38.2	1356	1	US-08-810-116-8	Sequence 8, Appli
30	2753	38.2	1356	2	US-07-930-548A-8	Sequence 8, Appli
31	2682	37.2	1367	2	US-08-443-861-2	Sequence 2, Appli
32	2682	37.2	1367	3	US-08-193-829B-2	Sequence 2, Appli
33	2665	37.0	1367	1	US-07-813-593-4	Sequence 4, Appli
34	2665	37.0	1367	1	US-07-977-451-6	Sequence 6, Appli
35	2665	37.0	1367	1	US-07-946-507-4	Sequence 4, Appli
36	2665	37.0	1367	1	US-08-252-517-6	Sequence 6, Appli
37	2665	37.0	1367	1	US-07-906-397A-6	Sequence 6, Appli

# RESULT 3

US-09-375-248-2

; Sequence 2, Application US/09375248  
; Patent No. 6764820  
; GENERAL INFORMATION:  
; APPLICANT: Ferrell, Robert E.  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Finegold, David N.  
; APPLICANT: Karkkainen, Marika  
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING  
; TITLE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)  
; FILE REFERENCE: 28967/35255A  
; CURRENT APPLICATION NUMBER: US/09/375,248  
; CURRENT FILING DATE: 1999-08-16  
; EARLIER APPLICATION NUMBER: PCT/US99/06133  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1363  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-248-2

Query Match 100.0%; Score 7211; DB 4; Length 1363;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 5

US-08-874-678-32

; Sequence 32, Application US/08874678  
; Patent No. 5952199  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

5-7-96

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/874,678  
; FILING DATE: HERewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63291-1/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1363 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-874-678-32

Query Match 99.3%; Score 7157; DB 2; Length 1363;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1354; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

RESULT 8

US-08-222-616-33

; Sequence 33, Application US/08222616  
; Patent No. 5635177  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/222,616  
; FILING DATE: 4-APR-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/00586  
; FILING DATE: 22-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/826935  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 821P2  
; TELECOMMUNICATION INFORMATION:



; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1298 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-222-616-33

Query Match 95.0%; Score 6852; DB 1; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

US-08-446-648-33

; Sequence 33, Application US/08446648  
; Patent No. 6331302

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Bennett, Brian D.  
; APPLICANT: Goeddel, David  
; APPLICANT: Lee, James M.  
; APPLICANT: Matthews, William  
; APPLICANT: Tsai, Siao Ping  
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES  
; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,648  
; FILING DATE:  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616  
; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1298 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-446-648-33

Query Match 95.0%; Score 6852; DB 3; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PGPUBS:

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7211	100.0	1363	10	US-09-375-248-2	Sequence 2, Appli
2	7211	100.0	1363	11	US-09-765-534B-4	Sequence 4, Appli
3	7211	100.0	1363	15	US-10-661-740-2	Sequence 2, Appli
4	7211	100.0	1363	16	US-10-774-802-4	Sequence 4, Appli
5	7211	100.0	1363	16	US-10-473-127-948	Sequence 948, App
6	7211	100.0	1363	16	US-10-473-127-950	Sequence 950, App
7	7211	100.0	1363	16	US-10-473-127-961	Sequence 961, App
8	7211	100.0	1363	16	US-10-473-127-963	Sequence 963, App
9	7167	99.4	1363	14	US-10-081-126-2	Sequence 2, Appli
10	7157	99.3	1363	14	US-10-105-901-32	Sequence 32, Appl
11	6852	95.0	1298	9	US-09-982-610-33	Sequence 33, Appl
12	6852	95.0	1298	11	US-09-765-534B-2	Sequence 2, Appli
13	6852	95.0	1298	14	US-10-262-538-32	Sequence 32, Appl
14	6852	95.0	1298	15	US-10-394-322A-67	Sequence 67, Appl
15	6852	95.0	1298	16	US-10-774-802-2	Sequence 2, Appli
16	6852	95.0	1298	16	US-10-669-176-32	Sequence 32, Appl
17	6852	95.0	1298	16	US-10-473-127-940	Sequence 940, App
18	6852	95.0	1298	16	US-10-473-127-958	Sequence 958, App
19	6852	95.0	1298	16	US-10-473-127-959	Sequence 959, App
20	6852	95.0	1298	16	US-10-473-127-960	Sequence 960, App
21	6852	95.0	1298	16	US-10-473-127-962	Sequence 962, App
22	6852	95.0	1298	16	US-10-473-127-973	Sequence 973, App
23	6852	95.0	1304	16	US-10-473-127-945	Sequence 945, App
24	6808	94.4	1298	15	US-10-165-193A-12	Sequence 12, Appl
25	6808	94.4	1298	16	US-10-326-048-4	Sequence 4, Appli
26	6808	94.4	1298	16	US-10-473-127-943	Sequence 943, App
27	6808	94.4	1298	16	US-10-473-127-964	Sequence 964, App
28	6808	94.4	1298	16	US-10-473-127-970	Sequence 970, App
29	6808	94.4	1298	17	US-10-781-581-222	Sequence 222, App
30	6797.5	94.3	1368	14	US-10-105-901-34	Sequence 34, Appl
31	6791	94.2	1298	16	US-10-473-127-949	Sequence 949, App
32	6320	87.6	1363	10	US-09-375-248-19	Sequence 19, Appl
33	6320	87.6	1363	15	US-10-661-740-19	Sequence 19, Appl
34	6320	87.6	1363	16	US-10-473-127-951	Sequence 951, App
35	6005.5	83.3	1362	14	US-10-105-901-33	Sequence 33, Appl
36	4135	57.3	777	14	US-10-105-901-3	Sequence 3, Appli
37	2762	38.3	1356	14	US-10-090-183-2	Sequence 2, Appli
38	2762	38.3	1356	15	US-10-394-322A-66	Sequence 66, Appl
39	2762	38.3	1356	15	US-10-440-464-129	Sequence 129, App
40	2762	38.3	1356	16	US-10-783-528-61	Sequence 61, Appl
41	2762	38.3	1356	17	US-10-872-198-115	Sequence 115, App
42	2762	38.3	1356	17	US-10-741-600-1469	Sequence 1469, Ap
43	2762	38.3	1356	17	US-10-741-600-1471	Sequence 1471, Ap
44	2762	38.3	1356	17	US-10-926-806-10	Sequence 10, Appl
45	2762	38.3	1356	20	US-11-021-951-115	Sequence 115, App

# RESULT 2

US-09-765-534B-4

; Sequence 4, Application US/09765534B

; Publication No. US20040037820A1

; GENERAL INFORMATION:

; APPLICANT: Alitalo, Kari

; APPLICANT: Kaipainen, Arja

; APPLICANT: Valtola, Reija

; APPLICANT: Jussila, Lotta

; TITLE OF INVENTION: Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapy

; FILE REFERENCE: 28113/34891

; CURRENT APPLICATION NUMBER: US/09/765,534B

; CURRENT FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 08/901,710

; PRIOR FILING DATE: 1997-07-28

; PRIOR APPLICATION NUMBER: 08/340,011

; PRIOR FILING DATE: 1994-11-14

; PRIOR APPLICATION NUMBER: 08/257,754

; PRIOR FILING DATE: 1994-07-09  
 ; PRIOR APPLICATION NUMBER: 07/959,951  
 ; PRIOR FILING DATE: 1992-10-09  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1363  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-765-534B-4

Query Match 100.0%; Score 7211; DB 11; Length 1363;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	6852	95.0	1298	2	A48999	protein-tyrosine k
2	6320	87.6	1363	2	I58375	protein-tyrosine k
3	4919.5	68.2	1379	2	JC4954	vascular endotheli
4	2804	38.9	1348	2	S51656	vascular endotheli
5	2753	38.2	1356	2	JC1402	protein-tyrosine k
6	2669	37.0	1367	2	A41228	protein-tyrosine k
7	2469	34.2	1333	2	I78875	receptor tyrosine
8	2463	34.2	1338	2	S09982	protein-tyrosine k
9	2444.5	33.9	1336	2	I60598	Fit-1 tyrosine kin
10	2437.5	33.8	1330	2	S49010	embryonic receptor
11	1283.5	17.8	367	2	B56598	endothelial kinase
12	1163.5	16.1	1089	1	PFHUGA	platelet-derived g
13	1151	16.0	1088	1	PFRTGA	platelet-derived g
14	1125	15.6	1089	1	S33727	platelet-derived g
15	1122.5	15.6	1087	2	I51552	platelet-derived g
16	1084	15.0	1106	1	PFHUGB	platelet-derived g
17	1052.5	14.6	1098	1	PFMSRB	platelet-derived g
18	1051	14.6	975	2	T30816	macrophage colony-
19	1044	14.5	978	1	A49814	protein-tyrosine k
20	1042.5	14.5	976	1	TVHUKT	protein-tyrosine k
21	1033.5	14.3	975	1	TVMSKT	protein-tyrosine k
22	1024	14.2	977	2	I45877	protein-tyrosine k
23	1021.5	14.2	960	1	JN0677	protein-tyrosine k
24	1018	14.1	954	2	I51703	c-kit-related kina
25	1012	14.0	1048	2	T30815	platelet-derived g
26	967	13.4	980	1	TVCTMD	macrophage colony-
27	956	13.3	941	1	TVMVMD	protein-tyrosine k
28	954.5	13.2	972	1	TVHUMD	macrophage colony-
29	954.5	13.2	992	2	A39931	protein-tyrosine k
30	951	13.2	1000	2	S18827	Flt3 protein - mou
31	949	13.2	978	2	S16385	macrophage colony-
32	930.5	12.9	976	1	TVMSMD	macrophage colony-
33	896	12.4	806	2	A35963	protein-tyrosine k
34	895.5	12.4	687	2	A49636	soluble vascular e
35	893.5	12.4	993	2	A36873	protein-tyrosine k
36	886.5	12.3	797	2	S38579	fibroblast growth
37	873	12.1	790	1	FOMVHZ	gag-kit polyprotei
38	869	12.1	822	1	TVHUFG	fibroblast growth
39	866	12.0	822	1	TVMSFG	fibroblast growth
40	865	12.0	814	1	A39752	fibroblast growth
41	863.5	12.0	822	2	B54846	fibroblast growth
42	862	12.0	822	2	S29840	fibroblast growth
43	862	12.0	832	2	JH0393	fibroblast growth
44	861.5	11.9	800	1	TVHU2F	fibroblast growth
45	861.5	11.9	800	2	A48991	heparin-binding gr

RESULT 1  
 A48999

protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human  
N;Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase 4  
C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A48999; A44930; G02316; S36130; A42010  
R;Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Alitalo, R.; Alitalo, K.  
Cancer Res. 52, 5738-5743, 1992  
A;Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and is expressed in multiple human tissues and cell lines.  
A;Reference number: A48999; MUID:93007958; PMID:1327515  
A;Accession: A48999  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1298 <PAJ>  
A;Cross-references: UNIPROT:P35916; PIDN:AAB23636.1; PID:g257352  
A;Experimental source: HEL erythroleukemia cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:115335)  
R;Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo, R.; Bailey, S.K.; McMahon, J.; Wasmuth, J.; Huebner, K.; Alitalo, K.  
Cancer Res. 52, 746-748, 1992  
A;Title: FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.  
A;Reference number: A44930; MUID:92119639; PMID:1310071  
A;Accession: A44930  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 761-1190 <APR>  
A;Cross-references: GB:X68203; NID:g31433  
A;Note: sequence extracted from NCBI backbone (NCBIP:78155)  
R;Wood, W.I.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: H01039  
A;Accession: G02316  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1298 <WOO>  
A;Cross-references: EMBL:U43143; NID:g1150990; PIDN:AAA85215.1; PID:g1150991  
R;Galland, F.  
submitted to the EMBL Data Library, December 1992  
A;Reference number: S36130  
A;Accession: S36130  
A;Molecule type: mRNA  
A;Residues: 1-23, 'D', 25-744, 'P', 746-751, 'RP', 754-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147-1163, 'D', 1165-1298 <GAL1>  
A;Cross-references: EMBL:X69878; NID:g297049; PIDN:CAA49505.1; PID:g297050  
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.  
Genomics 13, 475-478, 1992  
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.  
A;Reference number: A42010; MUID:92307693; PMID:1319394  
A;Accession: A42010  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 776-889, 'Q', 891-1127, 'V', 1129-1145, 'H', 1147-1163, 'D', 1165-1200 <GAL2>  
C;Genetics:  
A;Gene: GDB:FLT4  
A;Cross-references: GDB:128732; OMIM:136352  
A;Map position: 5q34-5q35  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane protein; tyrosine-specific protein kinase  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>  
F;843-1176/Domain: protein kinase homology <KIN>  
F;851-859/Region: protein kinase ATP-binding motif

Query Match 95.0%; Score 6852; DB 2; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 2.3e-301;  
Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLISISCRGQHLEWA	60
Db	1	MQRGAALCLRLWLCGLLDGLVSGYSMTPTLNITEESHVIDTGDSLISISCRGQHLEWA	60
Qy	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Db	61	WPGAQEAPATGDKDSEDGTVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Db	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKRSKSL	240
Db	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKRSKSL	240
Qy	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLSGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSFHALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNVV	420
Db	361	YPPPEFQWYKDGKALSGRHSFHALVLKEVTEASTGTYTLALWNSAAGLRRNISLELVNVV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQRSRLRRRQQQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWTCKMFAQRSRLRRRQQQ	480
Qy	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Db	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSHEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKYKLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKYKLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLLGACTKPQGFLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLLGACTKPQGFLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSES DVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080

Qy	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Db	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Qy	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMA PRSSQSSEEGSFS	1200
Db	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMA PRSSQSSEEGSFS	1200
Qy	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGS SRMKTFE EFP M	1260
Db	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGS SRMKTFE EFP M	1260
Qy	1261	TPTTYKGSVDNQTD SG MVLASEE FEQIESRHRQESGF	1297
Db	1261	TPTTYKGSVDNQTD SG MVLASEE FEQIESRHRQESGF	1297

## RESULT 2

I58375

protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Aug-2004

C;Accession: I58375; B42010

R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J.C.; Sookdeo, H.; Turner, K.J.; Wood, C.R.

Oncogene 8, 2293-2298, 1993

A;Title: Molecular cloning of murine FLT and FLT4.

A;Reference number: I58375; MUID:93330572; PMID:8393164

A;Accession: I58375

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1363 <RES>

A;Cross-references: UNIPROT:P35917; GB:L07296; NID:g293780; PIDN:AAA40077.1; PID:g293781

R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.

Genomics 13, 475-478, 1992

A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.

A;Reference number: A42010; MUID:92307693; PMID:1319394

A;Accession: B42010

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1033-1072 <GAL>

C;Genetics:

A;Gene: FTL4

C;Superfamily: protein kinase homology

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;843-1176/Domain: protein kinase homology <KIN>

F;851-859/Region: protein kinase ATP-binding motif

Query Match 87.6%; Score 6320; DB 2; Length 1363;  
Best Local Similarity 87.5%; Pred. No. 2.2e-277;  
Matches 1192; Conservative 68; Mismatches 103; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTPLNITEESHVIDTGDSLISICRGQHPLEWA	60
		:          :	
Db	1	MQPGAALNRLWLCLGLLQGLANGYSMTPTPLNITEDSYVIDTGDSLISICRGQHPLEWT	60
Qy	61	WPGAQEAPATGDKDSEDTGVVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYYKYIKARI	120
		:          :     :	
Db	61	WPGAQEVLTGKGKDETRVVDHCEGTEARPYCKVLLLAQTHANNTGSYHCYYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDAMWVPCLVSIPLNVTLSQSSSLWPDG	180
		:          :             :          :	
Db	121	EGTTAASTYVFVRDFKHPPINKPDTLLVNRKDSMWVPCLVSIPLNITLSQSSSALHPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPKSKL	240
		:                       :        :                    :	
Db	181	QEVLWDDRRGMVPTQLLRDALYLQCETTWGDQNFSLNLFVVHITGNELYDIQLYPKKSM	240
Qy	241	ELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTLSSILTIHNV	300

Db	241	ELLVGEKLVLNCTVWAEFDSGVTFDWDYPGKQAEAKWVPERRSQQTHTLSSILTIHNV	300
Qy	301	SQHDLGSYVCKANNGIQRFRESTEVIVHENPFISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQNDLGPYVCEANNGIQRFRESTEVIVHEKPFISVEWLKGPVLEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWYKDGKALSGRHSPhALVLKEVTEASTGTYTLALWNSAAGLRNNISLELVNV	420
Db	361	YPPPEFQWYKDRKAVTGRHNPhALVLKEVTEASAGVYTLALWNSAAGLRQNNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWPCKMFAQRLRRRQQQ	480
Db	421	PPHIHEKEASSPSIYSRHSRQTLTCTAYGVQPPLSVQWHWRPWPCKTFARSLRRRQQR	480
Qy	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVVSAMYKCVSVNKV	540
Db	481	DGMPQCRDWKEVTTQDAVNPIESLDTSWTEFVEGKNKTVSKLVIQDANVVSAMYKCVVNVK	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSZYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFSIESEPSDPLEGQSVRLSCRADNYTYEHLRWYRLNLSLTHD	600
Qy	601	AHGNNPLLLDCKNVHLFATPLAASLEEAPGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AQGNPLLLDCKNVHLFATPLEANLEEAEPGARHATLSLNI PRVAPEDEGDYVCEVQDRRS	660
Qy	661	HDKHKCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	QDKHKCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMRCPVAGAHVPSIVWYKDERLLEK	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILV	780
Db	721	ESGIDLADSNQRLSIQRVREEDAGRYLCSVCNAKGCNVSSASVAVEGSEDKGSMEIVILI	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMKRPAHADIKTGYSIIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRAIMSELKIL	900
Db	841	PRERLHLGRVLGHGAFGKVVEASAFGINKGSSCDTVAVKMLKEGATASEHRAIMSELKIL	900
Qy	901	IHIGNHLNVVNLGACTKPGQPLMVIVEFCKYGNLSNFLRAKRDASFPCAESPEQRGRF	960
Db	901	IHIGNHLNVVNLGACTKPNQPLMVIVEFCKYGNLSNFLRVKRDFTFNPAESPEQRRRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFAFBSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVEGAKADRRRPGSSDRALFTRFLMGKSARRAPLVQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSESDIVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Qy	1081	MAPESI FDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Db	1081	MAPESI FDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLKDGTRMRAPELA	1140
Qy	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMA PRSSQSSEEGSFS	1200
Db	1141	TPAIRHIMQSCWSGDPKARPAFSDLVEILGDLQGGGWQEEEEERMA LHSSQSSEEDGFM	1200
Qy	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFFPM	1260
Db	1201	QASTTALHIT EADADDSPPSMHCHSLAARYYNVVSFPGRLARGTKTPGSSRMKTFEELPM	1260
Qy	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGFSCKGPQNVAVTRAHPDSQGRRR	1320
Db	1261	TPTTYKASMDNOTDSGMVLASEEFEELSRHRPEGSFSCKGPQOHMDIPRGHPDPOGRRR	1320

Qy            1321 RPERGARGGQVFYNSEYGELSEPSSEEDHCSPSARVTFFTDNSY    1363  
             || :||:||:|||:|||:||| :|| | | || | ||| :||  
Db            1321 RPTGAAGGGKVFYNNEYGEVSQPCTEGDCPCSGSTFFADSSY    1363

Query Match 38.2%; Score 2753; DB 2; Length 1356;  
Best Local Similarity 43.9%; Pred. No. 1.1e-116;  
Matches 606; Conservative 205; Mismatches 480; Indels 88; Gaps 26;

Qy	1	MQRGAALCLRLWLCIGLLDGLVS--GYSMTPPTLNITEESHVIDTGDSLSISCRGQHPLE	58
		:   :       :   :     : :   :   :         :	
Db	1	MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDL	60
Qy	59	WAWPGAQEAPATGDKDSED TG VVRDC-EGTDARPYCKVLLLEHVHANDTGSYVCYYKYIK	117
		:   :   :   :   :       :   :   :	
Db	61	WLWPNNQSG-----SEQRVEVTECS DGL----FCKTLTIPKVI GNDTGAYKCFYR---	106
Qy	118	ARIEGTTAASSYVFVRDFEQPFINKPDT-----LLVNRKDMAMWVCLVSIPLNVTL--	169
		:     :   :     :   : :               :	
Db	107	---ETDLASVIYVYQDYRSPFIASVSDQHGVVYITENKNKTVVIPC LGSISNLNVSLCA	163
Qy	170	RSQSSVLWPDGQEVVWDDRRGMLVSTPLLHDALYLCETTWDQDFLSNPFLVHITGNEL	229
		:     : :   : :   :   : :   :   :   :	
Db	164	RYPEKRFVPDGNRISWDSKKGF TIPS YMISYAGMVFC EAKINDESYQSIMYIVVVVGYRI	223
Qy	230	YDIQLLPKRSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTH	289
		:     :                     :   :   :   :   :	
Db	224	YDVVLSPSHGIELSVGEKLVLNCTARTELVNGIDFNWEYPS SKHQHKKLVNRDLKTQSGS	283
Qy	290	ELS---SILTIHNVS OHDLGSYVCKANNGIORFRESTEVI VHENPFISVEWLKGPILEAT	346



Db	284	EMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEAT	343
Qy	347	AGDELVKLPVKLAAYPPPEFQWKDGKALSGRH---SPHALVLKEVTEASTGTYTLALWN	403
Db	344	VG-ERVRIPAKYLGYPPEIKWKYKNGI PLESNHTIKAGHVLTIMEVSEKDTGNYTVILT	402
Qy	404	SAAGLRRNISLELVVNVPQIHEKEASSP-SIYSRHSRQALTCTAYGVPLPLSIQWHWRP	462
Db	403	PISKEKQSHVSVLVVYVPPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHHIHWYQL	462
Qy	463	WTPCKMFAQRSLRRRQQQDLMPQCRDWRVTTQDAVNPIESLDTWTEFVEGKNKTVSKLV	522
Db	463	EEEC---ANEPSQAVSVTNYP-CEEWSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV	518
Qy	523	IQNANVSAMYKCVVSNKVGQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADS	582
Db	519	IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMPQTEQESVSLWCTADR	575
Qy	583	YKYEHLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEVAPGARHATLSL	638
Db	576	STFENLTWYKLGPPQLPIHVGEPLTPVCKNLDLTLWKLNATMFSNSTNDI-----LIM	627
Qy	639	SIPRVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQ	698
Db	628	ELKNASLQDQGDYVCLAQDRKTKKRHCVVRLTVLERVAPTITGNLENQTTSIGESIEVS	687
Qy	699	CLVAGAHAPSIVWYKDERLLEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVN	758
Db	688	CTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRVRKEDEGLYTQACSVLCAK	747
Qy	759	SSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMD	818
Db	748	VEAFFIIEGAQEKTNLEIIILVGTTVIAMFFWVLLVILGTVKRANGGELKTGYLSIVMD	807
Qy	819	PGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAV	878
Db	808	PDEPLDEHCERLPYDASKWEFPRDRLNLGKPLGRGAFGEIEADAFGIDKTATCRTVAV	867
Qy	879	KMLKEGATASEHRALMSELKILIHIGNHLNVNLLGACTKPGGPLMVIVEFCKYGNLSNF	938
Db	868	KMLKEGATHSEHRALMSELKILIHIGHHLNVNLLGACTKPGGPLMVIVEFCKFGNLSY	927
Qy	939	LRAKRDAFSPCAEKSPEQGRFRFRA---MVELARLDRRRPGSSDRVLFARFSKTEGGARRA	995
Db	928	LRSKRNEFVPTYKTG---ARFRQGDYVGAIPVDLKR--RLDSITSSQSSASSGFVEEK	981
Qy	996	S----PDQEA-EDLWLSPLTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDV	1050
Db	982	SLSDVEEEEPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV	1041
Qy	1051	VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL	1110
Db	1042	VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL	1101
Qy	1111	GASPYPGVQINEEFQRLRDGTRMRAPLATPAIRIMLNCWSGDPKARPAFSELVEILG	1170
Db	1102	GASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLG	1161
Qy	1171	DLQGRGLQEEEEVCMAPRS-SQSSEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAAR	1229
Db	1162	NLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSVPVSCMEEEVCDP-----KFH	1213
Qy	1230	YNNWVSFPGCLARGAETRGSRRMKTFFEEP-TPPTYKGSVDNQTDSGMVLASEEFEQIE	1288
Db	1214	YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTLE	1273
Qy	1289	SRHRQESGFSCCKPGQNVAVTRAHPDSQGRRRRPERGARGGQVFNSEYGESESEPSEED	1347
Db	1274	DRTKLSPSFGGMVPSK----SRESVAEGSNQ-----TSGYQSGYHSDDTTTVYSSEE	1323

## S09982

Query Match 34.2%; Score 2463; DB 2; Length 1338;  
Best Local Similarity 39.9%; Pred. No. 1.2e-103;  
Matches 547; Conservative 228; Mismatches 469; Indels 128; Gaps 28;

Qy	4	GAALCLRLWLCLGLLDGLVSGYSMTPTTLNITEESHVIDTGDSLISISCRGQHPLEAWP	63
Db	8	GVLLC-ALLSCL-LLTGSSSGSKLKDPELSLKGQTQHIMQAGQTLHLQCRGEAAHKWS---	62
Qy	64	AQEAPATGDKDSEDGTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARIEGT	123
Db	63	---LPEMVSKESERLSITKSACGRNGKQFCSTLTLTNAQANHGTGFYSCKYLAVPTSKKKE	119
Qy	124	TAASSYVFVRDFEQPFINK----PDTLLVNRKDDAMVWPCLVSIPLNVTLRS-QSSVLWP	178
Db	120	TESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELVI PCRVTSPNITVTLKKFPLDTLIP	179
Qy	179	DGQEVVWDDRRGMLVSTPLLDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLPRK	238
Db	180	DGKRIIWDSRKGFIIISNATYKEIGLLTCEATVNGHLYKTN-YLTHRQNTIIDVQISTPR	238
Qy	239	SLELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAEGRKWPERRSQQTHTELS---SIL	295
Db	239	PVKLLRGHTLVNLCTATTPLNTRVQMTWSYPDEKNKRAS--VRRRIDQSNSHANIFYSVL	296
Qy	296	TIHNVSQHDLGSYVCKANNGIQRFRESTEVIHVPFISVEWLKGFILEATAGDELVKLP	355
Db	297	TIDKMQNKDGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQVLETVAGKRSYRLS	356
Qy	356	VKLAAYPPPEFQWYKDGKALSGRHS-----PHALVLKEVTEASTGTYTLALWNSAAGLRR	410
Db	357	MKVKAFFSPPEVWLKDGLPATEKSARYLTRGYSLLIKDVTEEDAGNYTILLSIKQSNVFK	416
Qy	411	NISLELVNVPPQIHEKEASS---PSIYSRHSRQALCTAYGVPLPLSIQWHWRPWPCK	467
Db	417	NLTATLIVNVKPIYIEKAVSSFDPALYPLGSRQILCTAYGIPQP-TIKWFHPCNHNH	475
Qy	468	MFAQRSLRRRQQQDLMPQCRDRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQAN	527
Db	476	SEARCDFCSNNEESFILD-----ADSNMGNRIESITQRMALIEGKNKMASTLVVADSR	528
Qy	528	VSAMYKCVSVSNKVGQDERLIYFYVTTIPDGF--TIESKPSEELLEGQPVLLSCQADSYK	585

Db 529 ISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLKEMPT----EGEDLKLSCTVKNFLY 584

Qy 586 EHLRWYRL--NLSTLHDAHGNPLLLDCKNVHLFATPLAASLEEVAPGARHA-TLSLSIP 641  
: | | | | | : | : | : | : | : | : | : | : | : |

Db 585 RDVTWILLRTVNNRTMH-----YSISKQKMAITKEHSITLNLTIM 624

Qy 642 RVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQCLV 701  
| : : | | | : : : | | : | : | : | : | : | : |

Db 625 NVSLQDSGTYACRARNVYTGEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDDCHA 684

Qy 702 AGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSA 761  
| | | | | : | : : | : | : | : | : | : | : | : |

Db 685 NGVPEPQITWFKNNHKIQQEPGIILPGSSSTLFIERVTEEDEGVYHCKATNQKGSVESSA 744

Qy 762 SVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMDPGE 821  
: | : | : | : | : | : | : | : | : | : | : | : | : |

Db 745 YLTVQQTSDKSNLELITLTCTCVAATLFWLLLTLLIRKMKR-SSSEIKTDYLSIIMDPDE 803

Qy 822 VPLEEQCEYLSYDASQWEFPRERLHLGRVLGYAFGKVVEASAFGIHKSSCDTVAVKML 881  
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | |

Db 804 VPLDEQCERLPYDASKWEFARERLKLKSLGRGAFGKVQASAFGIKKSPTCRTVAVKML 863

Qy 882 KEGATASEHRALMSELKILIHGNHLNVNLLGACTKPGPLMVIVEFCKYGNLSNFLRA 941  
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | |

Db 864 KEGATASEYKALMTELKILTHIGHHLNVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKS 923

Qy 942 KRDAF---SPCAEKSPEQRGRFRAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPD 998  
| | | | : | : : : | : : : | : : : | : : : | : : : |

Db 924 KRDLFFLNKDAALHMEPKKEKMEPGLEQGGKPRLDVTSSESFASSGFQEDKSLSDVEEE 983

Qy 999 QEAEDLWLSPLTMEDLCVYSFQVARGMEFLASRKCIHRDLAARNILLSSEDVVKICDFGL 1058  
: : : : : | : | | | : | | | | | | | | | | | | : | | | | |

Db 984 EDSGDFYKEPITMEDLISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVMVKICDFGL 1043

Qy 1059 ARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGV 1118  
| | | | : | | | | | | | | | | | : | : | | | : | | | | | |

Db 1044 ARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVWSYGVLLWEIFSLGGSPYPGV 1103

Qy 1119 QINEEFQRLRDGTRMRAPELATPAIRIMLNCWSGDPKARPAFSELVEILGDLLQGRGL 1178  
| : : | : | | | | : | | : | : | | | | | : | | | | | |

Db 1104 QMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKERPRFAELVEKLGDLLQANVQ 1163

Qy 1179 QEEEEVCMAPRSSQSSEEGSFQVSTMALHIAQADAED-----SPPSLQRHSLAARYY 1231  
| : : : | : : : | : : : | : : : | : : : | : : : |

Db 1164 QDGKD--YIPINAILTGNSGFT-----YSTPAFSEDFFKESISAPKFNSGSSDDVRYV 1214

Qy 1232 NWVSFPGLCLARGAETRGSRRMKTFFBPMPTPTYKGSVDNQTDSGMVLAS---EEFEQIE 1288  
| | | : | | | : | | | : | | | : | | | : | | | : |

Db 1215 NAFKF-----MSLERIKTFEE--LLPNATSMFDDYQGDSSSTLLASPMKLRFTWTD 1262

Qy 1289 SRHR-----QESGFS-----CKGPGQNVAVTRAHPDSQGRRR 1320  
| : : : | | | : | : | : | : | : | : | : |

Db 1263 SKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSSCGHV-----SEGKRR 1306

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	7170	99.4	1363	2	Q86W07	Q86w07 homo sapien
2	6852	95.0	1298	1	VGR3_HUMAN	P35916 homo sapien
3	6811	94.5	1298	2	Q86W08	Q86w08 homo sapien
4	6320	87.6	1363	1	VGR3_MOUSE	P35917 mus musculu
5	6278	87.1	1363	2	Q91ZT1	Q91zt1 rattus norv
6	5085	70.5	1092	2	Q91ZT0	Q91zt0 rattus norv
7	4919.5	68.2	1379	2	P79701	P79701 coturnix co
8	2804	38.9	1348	1	VGR2_COTJA	P52583 coturnix co
9	2793	38.7	1348	2	Q677M1	Q677m1 gallus gall
10	2762	38.3	1356	1	VGR2_HUMAN	P35968 homo sapien

11	2681	37.2	1345	2	Q8VCD0	Q8vcd0	mus	musculu
12	2669	37.0	1367	1	VGR2_MOUSE	P35918	mus	musculu
13	2646	36.7	1343	1	VGR2_RAT	O08775	rattus	norv
14	2511	34.8	1327	2	Q8QHL3	Q8qhl3	gallus	gall
15	2469	34.2	1333	1	VGR1_MOUSE	P35969	mus	musculu
16	2463	34.2	1338	1	VGR1_HUMAN	P17948	h	vascular
17	2444.5	33.9	1336	1	VGR1_RAT	P53767	rattus	norv
18	2305	32.0	1302	1	VGR2_BRARE	Q8axb3	brachydanio	
19	1361	18.9	487	2	Q75WK4	Q75wk4	oryzias	lat
20	1283.5	17.8	367	2	Q91356	Q91356	coturnix	co
21	1181.5	16.4	1078	2	Q8AXC8	Q8axc8	fugu	rubrip
22	1163.5	16.1	1089	1	PGDS_HUMAN	P16234	homo	sapien
23	1160	16.1	1089	1	PGDS_MOUSE	P26618	mus	musculu
24	1158	16.1	1089	2	Q7TSJ3	Q7tsj3	mus	musculu
25	1151	16.0	1088	1	PGDS_RAT	P20786	rattus	norv
26	1150.5	16.0	1087	2	Q9PUF6	Q9puf6	gallus	
27	1134	15.7	1079	2	Q6E7G6	Q6e7g6	canis	famil
28	1128	15.6	404	2	Q9PUL0	Q9pul0	brachydanio	
29	1127	15.6	1474	2	Q8T4M0	Q8t4m0	drosophila	
30	1123.5	15.6	1087	2	Q7ZY71	Q7zy71	xenopus	lae
31	1122.5	15.6	1087	1	PGDS_XENLA	P26619	xenopus	lae
32	1118.5	15.5	1059	2	Q9DE49	Q9de49	brachydanio	
33	1117.5	15.5	1509	2	Q9VLQ8	Q9vlq8	drosophila	
34	1117	15.5	1461	2	Q8T9F6	Q8t9f6	drosophila	
35	1113.5	15.4	1503	2	Q7KTI8	Q7kti8	drosophila	
36	1110.5	15.4	1509	2	Q8IPG1	Q8ipg1	drosophila	
37	1107.5	15.4	1509	2	Q95P10	Q95p10	drosophila	
38	1106.5	15.3	1503	2	Q8T4L8	Q8t4l8	drosophila	
39	1105	15.3	1062	2	Q8AXC7	Q8axc7	fugu	rubrip
40	1084	15.0	1103	2	Q6QNF3	Q6qnf3	canis	famil
41	1084	15.0	1106	1	PGDR_HUMAN	P09619	homo	sapien
42	1071.5	14.9	992	2	Q8AXU0	Q8axu0	oncorhynchu	
43	1070.5	14.8	977	2	Q98SU1	Q98su1	danio	nigro
44	1070	14.8	1383	2	Q7Q840	Q7q840	anopheles	g
45	1065	14.8	977	2	Q98SU4	Q98su4	danio	albol

# RESULT 2

## VGR3\_HUMAN

ID VGR3\_HUMAN STANDARD; PRT; 1298 AA.

AC P35916;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)

DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).

GN Name=FLT4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND VARIANTS GLN-890 AND HIS-1146.

RC TISSUE=Placenta;

RX MEDLINE=93241723; PubMed=8386825;

RA Galland F., Karamysheva A., Pebusque M.-J., Borg J.-P., Rottapel R.,

RA Dubreuil P., Rosnet O., Birnbaum D.;

RT "The FLT4 gene encodes a transmembrane tyrosine kinase related to the

RT vascular endothelial growth factor receptor.";

RL Oncogene 8:1233-1240(1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93007958; PubMed=1327515;

RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,

RA Alitalo R., Alitalo K.;

RT "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like

RT loops and is expressed in multiple human tissues and cell lines.";

RL Cancer Res. 52:5738-5743(1992).

RN [3]

RP ERRATUM.

RA Pajusola K., Aprelikova O., Korhonen J., Kaipainen A., Pertovaara L.,  
 RA Alitalo R., Alitalo K.;  
 RL Cancer Res. 53:3845-3845(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lee J., Gray A., Yuan J., Luoh S.M., Avraham H., Wood W.I.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 761-1190 FROM N.A.  
 RX MEDLINE=92119639; PubMed=1310071;  
 RA Aprelikova O., Pajusola K., Partanen J., Armstrong E., Alitalo R.,  
 RA Bailey S.K., McMahon J., Wasmuth J., Huebner K., Alitalo K.;  
 RT "FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-  
 RT qter.";  
 RL Cancer Res. 52:746-748(1992).  
 RN [6]  
 RP SEQUENCE OF 25-39.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [7]  
 RP VARIANT HEREDITARY LYMPHEDEMA I LEU-1114.  
 RX PubMed=9817924; DOI=10.1093/hmg/7.13.2073;  
 RA Ferrell R.E., Levinson K.L., Esmen J.H., Kimak M.A., Lawrence E.C.,  
 RA Barmada M.M., Finegold D.N.;  
 RT "Hereditary lymphedema: evidence for linkage and genetic  
 RT heterogeneity.";  
 RL Hum. Mol. Genet. 7:2073-2078(1998).  
 RN [8]  
 RP INVOLVEMENT IN HEREDITARY LYMPHEDEMA I, AND CHARACTERIZATION OF  
 RP VARIANT HEREDITARY LYMPHEDEMA I ARG-1035.  
 RX PubMed=10856194;  
 RA Irrthum A., Karkkainen M.J., Devriendt K., Alitalo K., Vikkula M.;  
 RT "Congenital hereditary lymphedema caused by a mutation that  
 RT inactivates VEGFR3 tyrosine kinase.";  
 RL Am. J. Hum. Genet. 67:295-301(2000).  
 RN [9]  
 RP VARIANTS HEREDITARY LYMPHEDEMA I ARG-857; PRO-1041; PRO-1044 AND  
 RP LEU-1114, VARIANT SER-641, AND CHARACTERIZATION OF VARIANTS.  
 RX PubMed=10835628; DOI=10.1038/75997;  
 RA Karkkainen M.J., Ferrell R.E., Lawrence E.C., Kimak M.A.,  
 RA Levinson K.L., McTigue M.A., Alitalo K., Finegold D.N.;  
 RT "Missense mutations interfere with VEGFR-3 signalling in primary  
 RT lymphoedema.";  
 RL Nat. Genet. 25:153-159(2000).  
 RN [10]  
 RP VARIANTS JUVENILE HEMANGIOMA SER-954 AND SER-1137, AND VARIANTS  
 RP ALA-494; GLN-890 AND HIS-1146.  
 RX PubMed=11807987; DOI=10.1002/gcc.10028;  
 RA Walter J.W., North P.E., Waner M., Mizeracki A., Blei F.,  
 RA Walker J.W.T., Reinisch J.F., Marchuk D.A.;  
 RT "Somatic mutation of vascular endothelial growth factor receptors in  
 RT juvenile hemangioma.";  
 RL Genes Chromosomes Cancer 33:295-303(2002).  
 CC -!- FUNCTION: Receptor for VEGFC. Has a tyrosine-protein kinase  
 CC activity.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Placenta, lung, heart, and kidney, does not  
 CC seem to be expressed in pancreas and brain.  
 CC -!- DISEASE: Defects in FLT4 are the cause of hereditary lymphedema I  
 CC [MIM:153100]; also known as Nonne-Milroy lymphedema or Milroy  
 CC disease. Hereditary lymphedema is a chronic disabling condition  
 CC which results in swelling of the extremities due to altered  
 CC lymphatic flow. Patients with lymphedema suffer from recurrent  
 CC local infections and physical impairment. Hereditary lymphedema I  
 CC shows autosomal dominant inheritance and is characterized by onset  
 CC usually at birth.

CC -!- DISEASE: Defects in FLT4 are found in juvenile hemangioma.  
CC Juvenile hemangiomas are the most common tumors of infancy,  
CC occurring as many as 10/% of all births. These benign vascular  
CC lesions enlarge rapidly during the first year of life by  
CC hyperplasia of endothelial cells and attendant pericytes, and then  
CC spontaneously involute over a period of years, leaving loose  
CC fibrofatty tissue.  
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
CC receptor subfamily.  
CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
CC -----  
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CC -----  
DR EMBL; X69878; CAA49505.1; -.  
DR EMBL; X68203; CAA48290.1; ALT\_INIT.  
DR EMBL; U43143; AAA85215.1; -.  
DR PIR; A48999; A48999.  
DR HSSP; P35968; 1VR2.  
DR Genew; HGNC:3767; FLT4.  
DR MIM; 136352; -.  
DR MIM; 153100; -.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR011009; Kinase\_like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001824; RecepttyrkinsIII.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
DR InterPro; IPR009134; VEGFR.  
DR InterPro; IPR009137; VEGFR3.  
DR Pfam; PF00047; ig; 6.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR01832; VEGFRECEPTOR.  
DR PRINTS; PR01835; VEGFRECEPTR3.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00408; IGc2; 2.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS50835; IG\_LIKE; 6.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
KW ATP-binding; Direct protein sequencing; Disease mutation;  
KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Polymorphism;  
KW Receptor; Repeat; Signal; Transferase; Transmembrane;  
KW Tyrosine-protein kinase.  
FT SIGNAL 1 24  
FT CHAIN 25 1298 Vascular endothelial growth factor  
FT receptor 3.  
FT DOMAIN 25 775 Extracellular (Potential).  
FT TRANSMEM 776 797 Potential.  
FT DOMAIN 798 1298 Cytoplasmic (Potential).  
FT DOMAIN 30 127 Ig-like C2-type 1.  
FT DOMAIN 151 213 Ig-like C2-type 2.  
FT DOMAIN 219 326 Ig-like C2-type 3.  
FT DOMAIN 331 415 Ig-like C2-type 4.  
FT DOMAIN 422 552 Ig-like C2-type 5.  
FT DOMAIN 555 671 Ig-like C2-type 6.  
FT DOMAIN 678 764 Ig-like C2-type 7.  
FT DOMAIN 845 1173 Protein kinase.  
FT NP\_BIND 851 859 ATP (By similarity).  
FT BINDING 879 879 ATP (By similarity).

FT	ACT_SITE	1037	1037	By similarity.
FT	DISULFID	51	111	Potential.
FT	DISULFID	158	206	Potential.
FT	DISULFID	252	310	Potential.
FT	DISULFID	445	534	Potential.
FT	DISULFID	578	653	Potential.
FT	DISULFID	699	751	Potential.
FT	CARBOHYD	33	33	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	104	104	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	166	166	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	251	251	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	299	299	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	411	411	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	515	515	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	527	527	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	594	594	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	683	683	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	690	690	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	758	758	N-linked (GlcNAc. . .) (Potential).
FT	MOD_RES	1068	1068	Phosphotyrosine (by autocatalysis) (By similarity).
FT				
FT	VARIANT	494	494	T -> A.
FT				/FTid=VAR_018407.
FT	VARIANT	641	641	P -> S (does not affect kinase activity).
FT				/FTid=VAR_018408.
FT	VARIANT	857	857	G -> R (in hereditary lymphedema I; loss of kinase activity).
FT				

Query Match 95.0%; Score 6852; DB 1; Length 1298;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTLNITEESHVIDTGDLSLSISCRGQHPLEWA	60
Db	1	MQRGAALCLRLWLCLGLLDGLVSGYSMTPTLNITEESHVIDTGDLSLSISCRGQHPLEWA	60
Qy	61	WPGAQEAPATGDKDSEDGTGVVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYKYIKARI	120
Db	61	WPGAQEAPATGDKDSEDGTGVVRDCEGTDARPYCKVLLLEHVHANDTGSYVCYKYIKARI	120
Qy	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDMWVPCLVSIPLNVTLSQSSVLWPDG	180
Db	121	EGTTAASSYVFVRDFEQPFINKPDTLLVNRKDMWVPCLVSIPLNVTLSQSSVLWPDG	180
Qy	181	QEVVWDDRRGMLVSTPLLDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Db	181	QEVVWDDRRGMLVSTPLLDALYLQCETTWGDQDFLSNPFLVHITGNELYDIQLLPRKSL	240
Qy	241	ELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Db	241	ELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHNV	300
Qy	301	SQHDLGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Db	301	SQHDLGSYVCKANNGIQRFRESTEVIHNPFIISVEWLKGPILEATAGDELVKLPVKLAA	360
Qy	361	YPPPEFQWKDGKALSGRHSFHALVLKEVTEASTGTTLALWNSAAGLRRNISLELVNV	420
Db	361	YPPPEFQWKDGKALSGRHSFHALVLKEVTEASTGTTLALWNSAAGLRRNISLELVNV	420
Qy	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWPCKMFAQRSLLRRRQQQ	480
Db	421	PPQIHEKEASSPSIYSRHSRQALTCTAYGVPLPLSIQWHWRPWPCKMFAQRSLLRRRQQQ	480
Qy	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Db	481	DLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVIQANVNSAMYKCVVSNKV	540
Qy	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600
Db	541	GQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADSYKYEHLRWYRLNLSLTHD	600

Qy	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Db	601	AHGNPLLLDCKNVHLFATPLAASLEEVPAGARHATLSLSIPRVAPEHEGHYVCEVQDRRS	660
Qy	661	HDKHCHKKYLVSQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Db	661	HDKHCHKKYLVSQALEAPRLTQNLTDLLVNVSDSLEMQCLVAGAHAPSIVWYKDERLLEE	720
Qy	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Db	721	KSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNSSASVAVEGSEDKGSMEIVILV	780
Qy	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Db	781	GTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYSIIMDPGEVPLEEQCEYLSYDASQWEF	840
Qy	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Db	841	PRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVKMLKEGATASEHRALMSELKIL	900
Qy	901	IHIGNHLNVVNLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Db	901	IHIGNHLNVVNLGACTKPQGPLMVIVEFCKYGNLSNFLRAKRDAFSPCAEKSPEQRGRF	960
Qy	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Db	961	RAMVELARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSPLTMEDLVCYSFQ	1020
Qy	1021	VARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Db	1021	VARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSARLPLKW	1080
Qy	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Db	1081	MAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMRAPELA	1140
Qy	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS	1200
Db	1141	TPAIRRIMLNCWSGDPKARPAFSELVEILGDLQGRGLQEEEEVCMAPRSSQSSEEGSFS	1200
Qy	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFPM	1260
Db	1201	QVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTFEFPM	1260
Qy	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF	1297
Db	1261	TPTTYKGSVDNQTDSGMVLASEEFEQIESRHRQESGF	1297

# RESULT 10

VGR2\_HUMAN

ID VGR2\_HUMAN STANDARD; PRT; 1356 AA.  
AC P35968; O60723; Q14178;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
DE (VEGFR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase  
DE receptor Flk-1).  
GN Name=KDR; Synonyms=FLK1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yin L.Y., Wu Y., Patterson C.;  
RT "Full length human KDR/flk-1 sequence."  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]



RP SEQUENCE FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RA Yu Y., Whitney R.G., Sato J.D.;  
 RT "Coding region for human VEGF receptor KDR (VEGFR-2).";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 3-1356 FROM N.A.  
 RC TISSUE=Umbilical vein;  
 RX MEDLINE=92019839; PubMed=1656371;  
 RA Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,  
 RA Shows T.B.;  
 RT "Identification of a new endothelial cell growth factor receptor  
 RT tyrosine kinase.";  
 RL Oncogene 6:1677-1683(1991).  
 RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;  
 RA Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,  
 RA Harber E.;  
 RT "Cloning and functional analysis of the promoter for KDR/flk-1, a  
 RT receptor for vascular endothelial growth factor.";  
 RL J. Biol. Chem. 270:23111-23118(1995).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=93038639; PubMed=1417831;  
 RA Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,  
 RA Armellino D.C., Gospodarowicz D., Boehlen P.;  
 RT "Identification of the KDR tyrosine kinase as a receptor for vascular  
 RT endothelial cell growth factor.";  
 RL Biochem. Biophys. Res. Commun. 187:1579-1586(1992).  
 CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein  
 CC kinase activity. The VEGF-kinase ligand/receptor signaling system  
 CC plays a key role in vascular development and regulation of  
 CC vascular permeability.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC -----  
 DR EMBL; AF035121; AAB88005.1; -.  
 DR EMBL; AF063658; AAC16450.1; -.  
 DR EMBL; X61656; CAA43837.1; -.  
 DR EMBL; L04947; AAA59459.1; -.  
 DR EMBL; X89776; CAA61916.1; -.  
 DR PIR; JC1402; JC1402.  
 DR PDB; 1VR2; X-ray; A=806-1171.  
 DR Genew; HGNC:6307; KDR.  
 DR MIM; 191306; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001824; RecepttyrkinsIII.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR InterPro; IPR009134; VEGFR.  
 DR InterPro; IPR009136; VEGFR2.  
 DR Pfam; PF00047; ig; 6.

Pfam;	PF00069;	Pkinase;	1.
DR	PRINTS;	PRO1832;	VEGFRECEPTOR.
DR	PRINTS;	PRO1834;	VEGFRECEPTR2.
DR	ProDom;	PD000001;	Prot_kinase; 2.
DR	SMART;	SM00408;	IGc2; 2.
DR	SMART;	SM00219;	TyrKc; 1.
DR	PROSITE;	PS50835;	IG_LIKE; 5.
DR	PROSITE;	PS00107;	PROTEIN_KINASE_ATP; 1.
DR	PROSITE;	PS50011;	PROTEIN_KINASE_DOM; 1.
DR	PROSITE;	PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE;	PS00240;	RECEPTOR_TYR_KIN_III; 1.
KW	3D-structure;	Angiogenesis;	ATP-binding; Glycoprotein;
KW	Immunoglobulin domain;	Phosphorylation;	Receptor; Repeat; Signal;
KW	Transferase;	Transmembrane;	Tyrosine-protein kinase.
FT	SIGNAL	1	19 Potential.
FT	CHAIN	20	1356 Vascular endothelial growth factor receptor 2.
FT	DOMAIN	20	764 Extracellular (Potential).
FT	TRANSMEM	765	789 Potential.
FT	DOMAIN	790	1356 Cytoplasmic (Potential).
FT	DOMAIN	46	110 Ig-like C2-type 1.
FT	DOMAIN	141	207 Ig-like C2-type 2.
FT	DOMAIN	224	320 Ig-like C2-type 3.
FT	DOMAIN	328	414 Ig-like C2-type 4.
FT	DOMAIN	421	548 Ig-like C2-type 5.
FT	DOMAIN	551	660 Ig-like C2-type 6.
FT	DOMAIN	667	753 Ig-like C2-type 7.
FT	DOMAIN	834	1162 Protein kinase.
FT	NP_BIND	840	848 ATP (By similarity).
FT	BINDING	868	868 ATP (By similarity).
FT	ACT_SITE	1028	1028 By similarity.
FT	CARBOHYD	46	46 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	66	66 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	96	96 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	143	143 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	158	158 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	245	245 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	318	318 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	374	374 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	395	395 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	511	511 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	523	523 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	580	580 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	613	613 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	619	619 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	631	631 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	675	675 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	704	704 N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	721	721 N-linked (GlcNAc . . .) (Potential).
FT	MOD_RES	1059	1059 Phosphotyrosine (by autocatalysis) (By similarity).
FT	CONFLICT	2	2 Q -> E (in Ref. 2).
FT	CONFLICT	772	772 A -> T (in Ref. 3).
FT	CONFLICT	787	787 R -> G (in Ref. 3).
FT	CONFLICT	835	835 K -> N (in Ref. 3).
FT	CONFLICT	848	848 V -> E (in Ref. 3).
FT	CONFLICT	1347	1347 S -> T (in Ref. 3).
SQ	SEQUENCE	1356 AA;	151526 MW; 59E7C44B05CFEBB3 CRC64;
Query Match 38.3%; Score 2762; DB 1; Length 1356;			
Best Local Similarity 44.1%; Pred. No. 8.5e-172;			
Matches 608; Conservative 203; Mismatches 480; Indels 88; Gaps 26;			
Qy	1	MQRGAALCLRLWLCLGLLDGLVS--GYSMTPTPLNITEESHVIDTGDLSLSISCRGQHPLE	58
Db	1	MQSKVLLAVALWLCVETRAASVGLPSVSLDLPLRLSIQKDILTIKANTTLQITCRGQRLD	60
Qy	59	WAWPGAQAEAPATGDKDSED TG VVRDC-EGTDARPYKVL LLHEVHANDTGS YVCYKYIK	117
Db	61	WLWPNNQSG-----SEQRVEVTECS DGL----FCKTLTI PKVIGNDTGAYKCFYR---	106

Qy 118 ARIEGTTAASSYVFVRDFEQPFINKPDT-----LLVNRKDAMWVPCLVSIPLNVTL-- 169  
 | : ||:|: ||| : : : ||| || |||:  
 Db 107 ---ETDLASVIYVYQDYRSFPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCA 163

Qy 170 RSQSSVLWPDGQEVVWDDRRGMLVSTPLLDALYLQCETTWDQDFLSNPFLVHITGNEL 229  
 ||| : || :| : : : | : || : : | :| : :  
 Db 164 RYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFEAKINDESYQSIMYIVVVVGYRI 223

Qy 230 YDIQLLPKRSLELLVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTH 289  
 ||: | | : ||||| ||| | | : ||: || : : | | : :  
 Db 224 YDVVLSPSHGIELSVGEKLVNLCTARTELNVGIDFNWEYPSSKHQHKLVNRDLKTQSGS 283

Qy 290 ELS---SILTIHNVSQHDLGSYVCKANNGIQRFRETEVIVHENPFISVEWLKGPILEAT 346  
 |: ||| ||: | | | :||: : || | ||| ||: : |||  
 Db 284 EMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFSGSMESLVEAT 343

Qy 347 AGDELVKLPVKLAAYPPPEFQWKDGKALSGRH---SPHALVLKEVTEASTGTYTLLALWN 403  
 | | :|| | ||||| :|||: | | : | | : ||: | |||: |  
 Db 344 VG-ERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSRDGTGNYTVILT 402

Qy 404 SAAGLRRNISLELVNVPPQIHEKEASSP-SIYSRHSRQALTCTAYGVPLPLSIQWHWRP 462  
 : : : : ||| ||||| || | | : | |||| | : | | :|:  
 Db 403 PISKEKQSHVVSLLVYVPPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHIHVYWL 462

Qy 463 WTPCKMFAQSRLLRRRQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLV 522  
 | | : : : | | :||: | || : ||||| |||  
 Db 463 EEEC---ANEPSQAVSVTNPYP-CEEWSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV 518

Qy 523 IQNANVSAMYKCVVSNKVGQDERLIYFYVTTPDGFTIESKPSEELLEGQPVLLSCQADS 582  
 || |||||: ||| ||||: ||: | : | : | : | | ||  
 Db 519 IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMPQTEQESVSLWCTADR 575

Qy 583 KYEHLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEAPGARHATLSL 638  
 :||: ||: | | |||: | || : | : : | :  
 Db 576 STFENLTWYKLGPPQLPIHVGEPLTPVCKNLDTLWKLNATMFSNSTNDI-----LIM 627

Qy 639 SIPRVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQ 698  
 : : : : ||| ||||: :|| : | : | || : || : : :|:  
 Db 628 ELKNASLQDQGDYVCLAQDRKTKKRHCVVRLQTLVLERVAPTITGNLENQTTSIGESIEVS 687

Qy 699 CLVAGAHAPSIWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVN 758  
 | : | | :||: || | ||: | | : :||: ||| | | : ||  
 Db 688 CTASGNPPQIMWFKDNETLVEDSGIVLKDGNRNLTIIRVRKEDEGLYTCQACSVLGCAK 747

Qy 759 SSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMD 818  
 | :||: || :||: |||| ||||: ||||: ||||: ||||: ||||  
 Db 748 VEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMD 807

Qy 819 PGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYAFGKVVVEASAFGIHKSSCDTVAV 878  
 | ||: || | | ||||: ||||: ||| : || ||||: || ||| : |||  
 Db 808 PDELPLDEHCERLPYDASKWEFPRDLRLKLGKPLGRGAFQGVIEADAFPIDKTATCRTVAV 867

Qy 879 KMLKEGATASEHRALMSELKILIHIGNHLNVNLLGACTKPQGPLMVIVEFCKYGNLSNF 938  
 ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| :  
 Db 868 KMLKEGATHSEHRALMSELKILIHIGHHLNVNLLGACTKPGGPLMVIVEFCKFGNLSTY 927

Qy 939 LRAKRDAFSPCAEKSPEQGRGFRA---MVELARLDRRRPGSSDRVLFARFSKTEGGARRA 995  
 ||: ||: | | | ||| | : | : | : : : | :  
 Db 928 LRSKRNEFVPYKTKG---ARFRQGDYVGAI PVDLKR--RLDSITSSQSSASSGFVEEK 981

Qy 996 S----PDQEA-EDLWLSPLTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDV 1050  
 | :|| |||: ||: | :|||: ||||| ||||| ||||| ||||| :|  
 Db 982 SLSDVEEEEAPEDLYKDFTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV 1041

Qy 1051 VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL 1110  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1042 VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL 1101

Qy 1111 GASPYPGVQINEEFCQRLRDGTRMRAPELATPAIRIMLNCWSGDPKARPAFSELVEILG 1170  
 ||||| ||||: ||||: ||||: || : : ||: || | | ||||| ||  
 Db 1102 GASPYPGVKIDEFCRRLKEGTRMRAPDYTTPEMYQTMDCWHGEPSSQRPTFSELVEHLG 1161

Qy 1171 DLLQGRGLQEEEEVCMAPRS-SQSSEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAAR 1229  
 :||| : : : : : : : : : :  
 Db 1162 NLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEVCDP-----KFH 1213  
 Qy 1230 YYNWVSFPGCLARGAETRGSSRMKTFFEEFPM-TPTTYKGSVDNQTDSGMVLASEEFEQIE 1288  
 | | | :|||: : | ||||| : : |  
 Db 1214 YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLLEEPEVKVIPDDNQTDSGMVLASEELKTLE 1273  
 Qy 1289 SRHRQESGFSCCKPGQNVAVTRAHPDSQGRRRRPERGARGGQVFYNSEYGELSEPSEED 1347  
 | : | : : : | : | | : : : | :  
 Db 1274 DRTKLSPSPFGGMVPSK----SRESVASEGSNQ-----TSGYQSGYHSDDTDTTVYSSEE 1323

# RESULT 12

## VGR2\_MOUSE

ID VGR2\_MOUSE STANDARD; PRT; 1367 AA.  
 AC P35918;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
 DE (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase  
 DE 1) (Kinase NYK).  
 GN Name=Kdr; Synonyms=Flk-1, Flk1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Embryo;  
 RX MEDLINE=93208880; PubMed=7681362; DOI=10.1016/0092-8674(93)90573-9;  
 RA Millauer B., Wизigmann-Voos S., Schnurch H., Martinez R.,  
 RA Mueller N.P.H., Risau W., Ullrich A.;  
 RT "High affinity VEGF binding and developmental expression suggest Flk-1  
 RT as a major regulator of vasculogenesis and angiogenesis.";  
 RL Cell 72:835-846(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He; TISSUE=Fetal liver;  
 RX MEDLINE=92020984; PubMed=1717995;  
 RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,  
 RA Lemishcka I.R.;  
 RT "A receptor tyrosine kinase cDNA isolated from a population of  
 RT enriched primitive hematopoietic cells and exhibiting close genetic  
 RT linkage to c-kit.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93141255; PubMed=8423988;  
 RA Oelrichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.;  
 RT "NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from  
 RT E10 embryonic neuroepithelium is expressed in endothelial cells of the  
 RT developing embryo.";  
 RL Oncogene 8:11-18(1993).  
 RN [4]  
 RP SEQUENCE OF 1-15 FROM N.A.  
 RX MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;  
 RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,  
 RA Harber E.;  
 RT "Cloning and functional analysis of the promoter for KDR/flk-1, a  
 RT receptor for vascular endothelial growth factor.";  
 RL J. Biol. Chem. 270:23111-23118(1995).  
 RN [5]  
 RP FUNCTION.  
 RX MEDLINE=93361481; PubMed=8356051;  
 RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;  
 RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth

RT factor and is selectively expressed in vascular endothelium.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).

CC -!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein kinase activity. The VEGF-kinase ligand/receptor signaling system plays a key role in vascular development and regulation of vascular permeability.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung, kidney, brain and skeletal muscle, but is also expressed at lower levels in most other adult tissues.

CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

CC -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

CC -----

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CC -----

DR EMBL; X70842; CAA50192.1; -.

DR EMBL; X59397; CAA42040.1; -.

DR EMBL; S53103; AAB25043.1; -.

DR EMBL; X89777; CAA61917.1; -.

DR PIR; A41228; A41228.

DR HSSP; P35968; 1VR2.

DR MGD; MGI:96683; Kdr.

DR GO; GO:0045165; P:cell fate commitment; IMP.

DR GO; GO:0045446; P:endothelial cell differentiation; IDA.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig\_c2.

DR InterPro; IPR011009; Kinase\_like.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR001824; RecepttyrkinsIII.

DR InterPro; IPR001245; Tyr\_pkinase.

DR InterPro; IPR008266; Tyr\_pkinase\_AS.

DR InterPro; IPR009134; VEGFR.

DR InterPro; IPR009136; VEGFR2.

DR Pfam; PF00047; ig; 6.

DR Pfam; PF00069; Pkinase; 1.

DR PRINTS; PR01832; VEGFRECEPTOR.

DR PRINTS; PR01834; VEGFRECEPTR2.

DR ProDom; PD000001; Prot\_kinase; 2.

DR SMART; SM00408; IGc2; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS50835; IG\_LIKE; 5.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.

KW Angiogenesis; ATP-binding; Glycoprotein; Immunoglobulin domain;

KW Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane;

KW Tyrosine-protein kinase.

FT	SIGNAL	1	19	Potential.
FT	CHAIN	20	1367	Vascular endothelial growth factor receptor 2.
FT				Extracellular (Potential).
FT	DOMAIN	20	762	Potential.
FT	TRANSMEM	763	784	Cytoplasmic (Potential).
FT	DOMAIN	785	1367	Ig-like C2-type 1.
FT	DOMAIN	46	111	Ig-like C2-type 2.
FT	DOMAIN	143	209	Ig-like C2-type 3.
FT	DOMAIN	226	325	Ig-like C2-type 4.
FT	DOMAIN	330	416	Ig-like C2-type 5.
FT	DOMAIN	423	542	Ig-like C2-type 6.
FT	DOMAIN	549	656	Ig-like C2-type 7.
FT	DOMAIN	665	751	Protein kinase.
FT	DOMAIN	832	1160	

FT	NP_BIND	838	846	ATP (By similarity).
FT	BINDING	866	866	ATP (By similarity).
FT	ACT_SITE	1026	1026	By similarity.
FT	CARBOHYD	46	46	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	98	98	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	145	145	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	160	160	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	247	247	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	320	320	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	397	397	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	509	509	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	521	521	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	578	578	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	611	611	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	617	617	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	629	629	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	673	673	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	702	702	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	719	719	N-linked (GlcNAc. . .) (Potential).
FT	MOD_RES	1057	1057	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CONFLICT	25	25	P -> T (in Ref. 1).
FT	CONFLICT	679	679	G -> D (in Ref. 3).
FT	CONFLICT	783	784	LV -> VL (in Ref. 1).
FT	CONFLICT	917	917	S -> C (in Ref. 1).
FT	CONFLICT	1341	1367	QLTSCLNGSGPVPAPPPTPGNHERGAA -> RSPPV (in Ref. 3).
SQ	SEQUENCE	1367 AA;	152516 MW;	EFC99704F1DCA266 CRC64;

Query Match 37.0%; Score 2669; DB 1; Length 1367;  
 Best Local Similarity 43.0%; Pred. No. 1.1e-165;  
 Matches 588; Conservative 205; Mismatches 485; Indels 90; Gaps 24;

Qy	1	MQRGAALCLRLWLCLGLLDGLVS--GYSMTPPTLNITEESHVIDTGDLSISICRGQHPLE	58
Db	1	MESKALLAVALWFCVETRAASVGLPGDFLHPKPKLSTQKDILTILANTTLQITCRGQRDL	60
Qy	59	WAWPGAQEAPATGDKDSEDGTGVVRDCEGTDARPYCKVLLLEHVHANDTGSYVYKYIKA	118
Db	61	WLWPNAQ-----RDSEERVLVTECGGDS-IFCKTLTIPRVVGNLTGAYKCSYRDV--	110
Qy	119	RIEGTTAASSYVVRDFEQPFINKPDT-----LLVNRKDMWVPCLVSIPLNVTL--R	170
Db	111	----DIASTVYVVRDYRSPFIASVSDQHGIYITENKNKTVVIPCRGSISNLNVSLCAR	166
Qy	171	SQSSVLWPDGQEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNELY	230
Db	167	YPEKRFVPDGNRISWDSEIGFTLPSYMISYAGMVCFEAKINDETYQSIMYIVVVGYRIY	226
Qy	231	DIQLLPRKSLLELVGEKLVNLCTVWAEFNSGVTFDWDYPGKQAERGKWPERRSQQTHT	290
Db	227	DVILSPPEHIELSAGEKLVNLCTARTELVGLDFTWHSPPSKSHHKKIVNRDVKPFPGTV	286
Qy	291	LS---SILTIHNVSQHDLGSYVCKANNGIQRFRETEVIVHENPFISVEWLKGPILEATA	347
Db	287	AKMFLSTLTIESVTKSDQGEYTCVASSGRMIKRNTFVRVHTKPFIAFGSGMKSLVEATV	346
Qy	348	GDELVKLPVKLAAYPPPEFQWYKDGKALSGRHS---PHALVLKEVTEASTGTYYTLALWNS	404
Db	347	GSQ-VRIPVKYLSPAPDIKWYRNGRPIESNYTMIVGDELTIMEVTERDAGNYTVILTNP	405
Qy	405	AAGLRNINISLELVNVPPQIHEKEASSP-SIYSRHSRQALTCTAYGVPLPLSIQWHWRPW	463
Db	406	ISMEKQSHMVSLLVNVPPQIGEKALISPMDSYQYGTMTLTCTVYANPPLHHIQWYQLE	465
Qy	464	TPCKMFAQRSLRRRQQQLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLVI	523
Db	466	EACSY-----RPGQTSFYACKERHVEDFQGGNKIEVTKNQYALIEGKNKTVSTLVI	517
Qy	524	QNANVSAMKYCVVSNKVGQDERLIYFYVTTIPDGFITIESKPSEELLEGGQPVLLSCQADSY	583

Db	518	QAANVSALYKCEAINKAGRGERSVISFHVIRGPE---ITVQPAAQPTQESVSLCTADRN	574
Qy	584	KYEHRLRWYRLNLSTLHDAHGNPLLLDCKNV---HLFATPLAASLEEVAPGARHATLSLS	639
Db	575	TFENLTWYKLGSQLTSVHMGESLTPVCKNLDALWKLNGTMFSNSTNDI-----LIVA	626
Qy	640	IPRVAPEHEGHYVCEVQDRRSHDKHCHKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQC	699
Db	627	FQNASLQDQGDYVCSAQDKKTKKRHCLVKQLIILERMAMPITGNLENQTTTIGETIEVTC	686
Qy	700	LVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSVCNAKGCVNS	759
Db	687	PASGNPTPHITWFKDNETLVEDSGIVLRDGNRNLTIRRVKEDGGLYTCQACNVLCARA	746
Qy	760	SASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTYLSIIMDP	819
Db	747	ETLFIIEGAQEKTNLEVIILVGTAVIAMFFWVLLLLVILVRTVKRANEGELKTGYLSIVMDP	806
Qy	820	GEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKGSSCDTVAVK	879
Db	807	DEPLDERCERLPYDASKWEFPRDLKLGKPLGRGAFGQVIEADAFGIDKTATCKTVAVK	866
Qy	880	MLKEGATASEHRALMSELKILIHIGNHLNVNLLGACTKPGPLMVIVEFCKYGNLSNFL	939
Db	867	MLKEGATHSEHRALMSELKILIHIGHHLNVNLLGACTKPGGPLMVIVEFSKFGNLSTYL	926
Qy	940	RAKRDAFSPCAEKSPEQRGRFRA---MVELARLDRRRPGSSDRVLFARFSKTEGGARRA	995
Db	927	RGKRNEFVVPYKSKG---ARFRQGDYVGELS-VDLKR--RLDSITSSQSSASSGFVEEK	979
Qy	996	S-----PDQEAEDLWLSPLTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSSESDV	1050
Db	980	SLSDVEEEEASEELYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSSEKNV	1039
Qy	1051	VKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSL	1110
Db	1040	VKICDFGLARDIYKDPDYVRKG DARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL	1099
Qy	1111	GASPYPGVQINEEFCQRLRDGTRMRAPELATPAIRRIMLNCWSGDPKARPAFSELVEILG	1170
Db	1100	GASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMDCWHEDPNQRPSFSELVEHLG	1159
Qy	1171	DLQGRGLQEEEEVCMAPRS-SQSSEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAAR	1229
Db	1160	NLLQANAQQDGKDYIVLPMSETLSMEEDSGLSLPTSPVSCMEEEEVCDP-----KPH	1211
Qy	1230	YYNWVSFPGCLARGAETRGSRRMKTFFEEFPM-TPTTYKGSVDNQTDSGMVLASEEFEQIE	1288
Db	1212	YDNTAGISHYLQNSKRKSRPVSVKTFEDIPLLEEPEVKVIPDDSQTDSGMVLASEELKTLE	1271
Qy	1289	SRHRQESGFSCKPGQNVAVTRAHPDSQGRRRRPERGARGGQVFYNSE	1336
Db	1272	DRNKLSPSFG---GMMPKSRESVASEGSNQ-----TSGYQSGYHSD	1310